

RESULT 1

TMS5_HUMAN

ID TMS5_HUMAN STANDARD; PRT; 457 AA.

AC Q9H3S3;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Transmembrane protease, serine 5 (EC 3.4.21.-) (Spinesin).

GN TMPRSS5.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX PubMed=11741986;

RA Yamaguchi N., Okui A., Yamada T., Nakazato H., Mitsui S.;

RT "Spinesin/TMPRSS5, a novel transmembrane serine protease, cloned from human spinal cord.";

RL J. Biol. Chem. 277:6806-6812(2002).

CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).

CC -!- TISSUE SPECIFICITY: Brain-specific. Predominantly expressed in neurons, in their axons, and at the synapses of motoneurons in the spinal cord.

CC -!- SIMILARITY: Belongs to peptidase family S1.

CC -!- SIMILARITY: Contains 1 SRCR domain.

CC -----
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DR EMBL; AB028140; BAB20375.1; -.

DR HSSP; P00763; 1DPO.

DR Genew; HGNC:14908; TMPRSS5.

DR MIM; 606751; -.

DR MEROPS; S01.313; -.

DR InterPro; IPR009003; Cys_Ser_trypsin.

DR InterPro; IPR001254; Peptidase_S1.

DR InterPro; IPR001314; Peptidase_S1A.

DR InterPro; IPR001190; Srcr_receptor.

DR Pfam; PF00089; trypsin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR SMART; SM00020; Tryp_SPc; 1.

DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

DR PROSITE; PS00420; SRCR_1; FALSE_NEG.

DR PROSITE; PS50287; SRCR_2; FALSE_NEG.

KW Hydrolase; Serine protease; Transmembrane; Signal-anchor;

KW Glycoprotein.

FT DOMAIN 1 49 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 50 70 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

RESULT 1

S00845

hepsin (EC 3.4.21.-) - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999

C;Accession: S00845

R;Leytus, S.P.; Loeb, K.R.; Hagen, F.S.; Kurachi, K.; Davie, E.W.

Biochemistry 27, 1067-1074, 1988

A;Title: A novel trypsin-like serine protease (hepsin) with a putative transmembrane domain expressed by human liver and hepatoma cells.

A;Reference number: S00845; MUID:88209431; PMID:2835076

A;Accession: S00845

A;Molecule type: mRNA

A;Residues: 1-417 <LEY>

A;Cross-references: EMBL:X07732; NID:g32063; PIDN:CAA30558.1; PID:g32064

C;Genetics:

A;Gene: GDB:HPN; TMPRSS1; hepsin

A;Cross-references: GDB:135685; OMIM:142440

A;Map position: 19q11-19q13.2

C;Superfamily: hepsin; trypsin homology

C;Keywords: hydrolase; liver; serine proteinase; transmembrane protein

F;23-45/Domain: transmembrane #status predicted <TMN>

F;163-400/Domain: trypsin homology <TRY>

F;188-204,291-359,322-338,349-381/Disulfide bonds: #status predicted

F;203,257,353/Active site: His, Asp, Ser #status predicted

Query Match 24.3%; Score 602.5; DB 1; Length 417;
Best Local Similarity 33.3%; Pred. No. 2.9e-41;
Matches 139; Conservative 61; Mismatches 155; Indels 63; Gaps 11;

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Qy      53 GALGLLAGAGVGSWLLVLYLCPAASQPISGTLQDEEITLSCSEASAEELLPALPKTVSF 112
      | | | | | | | | | | : | | : : | : | | | | |
Db      24 GTLLLLTAIGAASWAIVALLRSDQEPLYPV-----QVSSADARLMVFDKT--- 69

Qy     113 RINSEDFLLEAQVRDQPRWLLVCHGWSPALGLQICWSLGHRLRLTHHKGVNLTDIKLNSS 172
      : | | : | : : | : | | | : : | :
Db      70 -----EGTWRLLCSSRSNARVAGLSCEEMGFLRALTHSEL DVRTAGANGT 114

Qy     173 QEFAQLSPRLLGGFLEEAWQPRN-----NCTSGQVSLRCSECGARPL-ASRIVGG 221
      | : : | | : | | : | : | : | | | | |
Db     115 SGFF-----CVDEGRLPHTQRLLEVISVDCPRGRFLAAICQDCGRRKLPVDRIVGG 166

Qy     222 QSVAPGRWPWQASVALGFRHTCGGSVLAPRWVVTAAHCMHSFRLARLSSWRVHAGLVSHS 281
      : : | | | | | | : | | | | : | : | | | | : :
Db     167 RDTSLGRWPWQVSLRYDGAHLCCGGSLLSGDWVLTAAHCFPE-RNRVLSRWRVFAGAVAQA 225

Qy     282 AVRPHQGAL-VERIIPHPHY-----SAQNHDYDVALLRLQTALNFSDTVGAVCLPAKEQ 334
      : | | | | : : : | : : : | : | : | : : | | | |
Db     226 S--PHGLQLGVQAVVYHGGYLPFRDPNSEENSNDIALVHLSSPLPLTEYIQPVCLPAAGQ 283

Qy     335 HFPKGSRCWVSGWGHTPSHTYSSDMLQDTVVPFLFSTQLCNSSCVYSGALTTPRMLCAGYL 394
      | | | : | | : : : | : | : | : | : | : | | |
Db     284 ALVDGKICTVTGWGNTQ-YYGQQAGVLQEARVPIISNDVCNGADFYGNQIKPKMFCAGYP 342

Qy     395 DGRADACQGDSSGGPLVCPDG----DTWRLVGVVSWGRACAEPNHPGVYAKVAEFLDWI 448
      : | | | | | | | | | | | | | | : | : | | | | |
Db     343 EGGIDACQGDSSGGPFVCEDSISRTPRWRLCGIVSWGTCALAQKPGVYTKVSDFREWI 400

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US-10-607-565-108

Query Match 91.9%; Score 2280; DB 12; Length 480;
Best Local Similarity 99.8%; Pred. No. 2.9e-198;
Matches 420; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

[illegible]

Db

480 L 480